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**RAW SEQUENCE LISTING**

DATE: 08/07/2002

PATENT APPLICATION: US/09/663,542

TIME: 15:51:49

Input Set : A:\PC10349AGPR Seq List.ST25.txt

Output Set: N:\CRF3\08072002\I663542.raw

#11

3 <110> APPLICANT: Pfizer Inc.  
 4       Fidock, Mark D.  
 5       Robas, Nicola M.  
 7 <120> TITLE OF INVENTION: Phosphodiesterase Enzymes  
 9 <130> FILE REFERENCE: PC10349AGPR  
 11 <140> CURRENT APPLICATION NUMBER: 09/663,542  
 12 <141> CURRENT FILING DATE: 2000-09-15  
 14 <150> PRIOR APPLICATION NUMBER: US 60/177,517  
 15 <151> PRIOR FILING DATE: 2000-01-21  
 17 <150> PRIOR APPLICATION NUMBER: GB 9922124.4  
 18 <151> PRIOR FILING DATE: 1999-09-17  
 20 <160> NUMBER OF SEQ ID NOS: 16  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 684  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
 29 <400> SEQUENCE: 1  
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 36                               20                               25                               30  
 39 Ala Ser Leu Ala Glu Lys Gln Glu Lys His Gln Asp Phe Leu Ile Gln  
 40                               35                               40                               45  
 43 Arg Gln Thr Lys Thr Lys Asp Arg Arg Phe Asn Asp Glu Ile Asp Lys  
 44                               50                               55                               60  
 47 Leu Thr Gly Tyr Lys Thr Lys Ser Leu Leu Cys Met Pro Ile Arg Ser  
 48 65                               70                               75                               80  
 51 Ser Asp Gly Glu Ile Ile Gly Val Ala Gln Ala Ile Asn Lys Ile Pro  
 52                               85                               90                               95  
 55 Glu Gly Ala Pro Phe Thr Glu Asp Asp Glu Lys Val Met Gln Met Tyr  
 56                               100                               105                               110  
 59 Leu Pro Phe Cys Gly Ile Ala Ile Ser Asn Ala Gln Leu Phe Ala Ala  
 60                               115                               120                               125  
 63 Ser Arg Lys Glu Tyr Glu Arg Ser Arg Ala Leu Leu Glu Val Val Asn  
 64                               130                               135                               140  
 67 Asp Leu Phe Glu Glu Gln Thr Asp Leu Glu Lys Ile Val Lys Lys Ile  
 68 145                               150                               155                               160  
 71 Met His Arg Ala Gln Thr Leu Leu Lys Cys Glu Arg Cys Ser Val Leu  
 72                               165                               170                               175  
 75 Leu Leu Glu Asp Ile Glu Ser Pro Val Val Lys Phe Thr Lys Ser Phe  
 76                               180                               185                               190  
 79 Glu Leu Met Ser Pro Lys Cys Ser Ala Asp Ala Glu Asn Ser Phe Lys

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84          210          215          220
87 Ile Ala Glu Leu Val Ala Ser Thr Gly Leu Pro Val Asn Ile Ser Asp
88 225          230          235          240
91 Ala Tyr Gln Asp Pro Arg Phe Asp Ala Glu Ala Asp Gln Ile Ser Gly
92          245          250          255
95 Phe His Ile Arg Ser Val Leu Cys Val Pro Ile Trp Asn Ser Asn His
96          260          265          270
99 Gln Ile Ile Gly Val Ala Gln Val Leu Asn Arg Leu Asp Gly Lys Pro
100          275          280          285
103 Phe Asp Asp Ala Asp Gln Arg Leu Phe Glu Ala Phe Val Ile Phe Cys
104          290          295          300
107 Gly Leu Gly Ile Asn Asn Thr Ile Met Tyr Asp Gln Val Lys Lys Ser
108 305          310          315          320
111 Trp Ala Lys Gln Ser Val Ala Leu Asp Val Leu Ser Tyr His Ala Thr
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115 Cys Ser Lys Ala Glu Val Asp Lys Phe Lys Ala Ala Asn Ile Pro Leu
116          340          345          350
119 Val Ser Glu Leu Ala Ile Asp Asp Ile His Phe Asp Asp Phe Ser Leu
120          355          360          365
123 Asp Val Asp Ala Met Ile Thr Ala Ala Leu Arg Met Phe Met Glu Leu
124          370          375          380
127 Gly Met Val Gln Lys Phe Lys Ile Asp Tyr Glu Thr Leu Cys Arg Trp
128 385          390          395          400
131 Leu Leu Thr Val Arg Lys Asn Tyr Arg Met Val Leu Tyr His Asn Trp
132          405          410          415
135 Arg His Ala Phe Asn Val Cys Gln Leu Met Phe Ala Met Leu Thr Thr
136          420          425          430
139 Ala Gly Phe Gln Asp Ile Leu Thr Glu Val Glu Ile Leu Ala Val Ile
140          435          440          445
143 Val Gly Cys Leu Cys His Asp Leu Asp His Arg Gly Thr Asn Asn Ala
144          450          455          460
147 Phe Gln Ala Lys Ser Gly Ser Ala Leu Ala Gln Leu Tyr Gly Thr Ser
148 465          470          475          480
151 Ala Thr Leu Glu His His His Phe Asn His Ala Val Met Ile Leu Gln
152          485          490          495
155 Ser Glu Gly His Asn Ile Phe Ala Asn Leu Ser Ser Lys Glu Tyr Ser
156          500          505          510
159 Asp Leu Met Gln Leu Leu Lys Gln Ser Ile Leu Ala Thr Asp Leu Thr
160          515          520          525
163 Leu Tyr Phe Glu Arg Arg Thr Glu Phe Phe Glu Leu Val Ser Lys Gly
164          530          535          540
167 Glu Tyr Asp Trp Asn Ile Lys Asn His Arg Asp Ile Phe Arg Ser Met
168 545          550          555          560
171 Leu Met Thr Ala Cys Asp Leu Gly Ala Val Thr Lys Pro Trp Glu Ile
172          565          570          575
175 Ser Arg Gln Val Ala Glu Leu Val Thr Ser Glu Phe Phe Glu Gln Gly
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179 Asp Arg Glu Arg Leu Glu Leu Lys Leu Thr Pro Ser Ala Ile Phe Asp
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183 Arg Asn Arg Lys Asp Glu Leu Pro Arg Leu Gln Leu Glu Trp Ile Asp
184      610      615      620
187 Ser Ile Cys Met Pro Leu Tyr Gln Ala Leu Val Lys Val Asn Val Lys
188 625      630      635      640
191 Leu Lys Pro Met Leu Asp Ser Val Ala Thr Asn Arg Ser Lys Trp Glu
192      645      650      655
195 Glu Leu His Gln Lys Arg Leu Leu Ala Ser Thr Ala Ser Ser Ser
196      660      665      670
199 Pro Ala Ser Val Met Val Ala Lys Glu Asp Arg Asn
200      675      680
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204 <211> LENGTH: 2078
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 2
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211 agtggaaaaa ggtgaaaatc acaagactgg tccaaatctc tggggcctct ttggctgaaa      120
213 aacaggaaaa gcaccaggat tttcttatac agaggcaaac aaaaacaaag gatcgacgat      180
215 tcaatgatga aatcgacaag ctgactggat acaagacaaa atcattattg tgcattgcta      240
217 tccgaagcag tgatgggtgag attattgggtg tggcccaagc gataaataag attcctgaag      300
219 gagctccatt tactgaagat gatgaaaaag ttatgcagat gtatcttcca ttttgtggaa      360
221 tcgccatata taacgctcag ctctttgctg cctcaaggaa agaatatgaa agaagcagag      420
223 ctttgctaga ggtgggttaat gacctctttg aagaacagac tgacctggag aaaattgtca      480
225 agaaaaataat gcacggggcc caaactctgc tgaaatgtga gcgctgttct gttttactcc      540
227 tagaggacat cgaatcacca gtggtgaaat ttaccaaatc ctttgaattg atgtcccca      600
229 agtgcagtgc tgatgctgag aacagtttca aagaaagcat ggagaaatca tcatactccg      660
231 actggctaataaataacagc attgctgagc tggttgcttc aacaggcctt ccagtgaaca      720
233 tcagtgatgc ctaccaggat ccgcgctttg atgcagaggc agaccagata tctggttttc      780
235 acataagatc tgttctttgt gtccctatctt ggaatagcaa ccaccaaata attggagtgg      840
237 ctcaagtgtt aaacagactt gatgggaaac cttttgatga tgcagatcaa cgactttttg      900
239 aggcctttgt catcttttgt ggacttggca tcaacaacac aattatgtat gatcaagtga      960
241 agaagtcttg ggccaagcag tctgttgctc ttgatgtgct atcataccat gcaacatgtt      1020
243 caaaagctga agttgacaag tttaaggcag ccaacatccc tctggtgtca gaacttgcca      1080
245 tcgatgacat tcattttgat gacttttctc tcgacgttga tgccatgatc acagctgctc      1140
247 tccggatgtt catggagctg gggatggtac agaaatttaa aattgactat gagacactgt      1200
249 gtaggtggtt tttgacagtg aggaaaaact atcggatggt tctataccac aactggagac      1260
251 atgccttcaa cgtgtgtcag ctgatgttcg cgatgttaac cactgctggg tttcaagaca      1320
253 ttctgaccga ggtggaaatt ttagecgtga ttgtgggatg cctgtgtcat gacctcgacc      1380
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259 agggtcacaa tatcttttgt aacctgtcct ccaaggataa tagtgacctt atgcagcttt      1560
261 tgaagcagtc aatattggca acagacctca cgctgtactt tgagaggaga actgaattct      1620
263 ttgaacttgt cagtaaagga gaatacgatt ggaacatcaa aaaccatcgt gatataattc      1680
265 gatcaatgtt aatgacagcc tgtgaccttg gagcctgtac caaaccgtgg gagatctcca      1740
267 gacaggtggc agaacttgta accagtgagt tcttcgaaca aggagatcgg gagagattag      1800
269 agctcaaaact cactccttca gcaatttttg atcggaaccg gaaggatgaa ctgcctcggt      1860
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273 acgtgaaact gaagccgatg ctagattcag tagctacaaa cagaagtaag tgggaagagc 1980
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292 20 25 30
295 Glu Val Val Asn Asp Leu Phe Glu Glu Gln Thr Asp Leu Glu Lys Ile
296 35 40 45
299 Val Lys Lys Ile Met His Arg Ala Gln Thr Leu Leu Lys Cys Glu Arg
300 50 55 60
303 Cys Ser Val Leu Leu Leu Glu Asp Ile Glu Ser Pro Val Val Lys Phe
304 65 70 75 80
307 Thr Lys Ser Phe Glu Leu Met Ser Pro Lys Cys Ser Ala Asp Ala Glu
308 85 90 95
311 Asn Ser Phe Lys Glu Ser Met Glu Lys Ser Ser Tyr Ser Asp Trp Leu
312 100 105 110
315 Ile Asn Asn Ser Ile Ala Glu Leu Val Ala Ser Thr Gly Leu Pro Val
316 115 120 125
319 Asn Ile Ser Asp Ala Tyr Gln Asp Pro Arg Phe Asp Ala Glu Ala Asp
320 130 135 140
323 Gln Ile Ser Gly Phe His Ile Arg Ser Val Leu Cys Val Pro Ile Trp
324 145 150 155 160
327 Asn Ser Asn His Gln Ile Ile Gly Val Ala Gln Val Leu Asn Arg Leu
328 165 170 175
331 Asp Gly Lys Pro Phe Asp Asp Ala Asp Gln Arg Leu Phe Glu Ala Phe
332 180 185 190
335 Val Ile Phe Cys Gly Leu Gly Ile Asn Asn Thr Ile Met Tyr Asp Gln
336 195 200 205
339 Val Lys Lys Ser Trp Ala Lys Gln Ser Val Ala Leu Asp Val Leu Ser
340 210 215 220
343 Tyr His Ala Thr Cys Ser Lys Ala Glu Val Asp Lys Phe Lys Ala Ala
344 225 230 235 240
347 Asn Ile Pro Leu Val Ser Glu Leu Ala Ile Asp Asp Ile His Phe Asp
348 245 250 255
351 Asp Phe Ser Leu Asp Val Asp Ala Met Ile Thr Ala Ala Leu Arg Met
352 260 265 270
355 Phe Met Glu Leu Gly Met Val Gln Lys Phe Lys Ile Asp Tyr Glu Thr
356 275 280 285
359 Leu Cys Arg Trp Leu Leu Thr Val Arg Lys Asn Tyr Arg Met Val Leu
360 290 295 300
363 Tyr His Asn Trp Arg His Ala Phe Asn Val Cys Gln Leu Met Phe Ala
364 305 310 315 320
367 Met Leu Thr Thr Ala Gly Phe Gln Asp Ile Leu Thr Glu Val Glu Ile

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368          325          330          335
371 Leu Ala Val Ile Val Gly Cys Leu Cys His Asp Leu Asp His Arg Gly
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375 Thr Asn Asn Ala Phe Gln Ala Lys Ser Gly Ser Ala Leu Ala Gln Leu
376          355          360          365
379 Tyr Gly Thr Ser Ala Thr Leu Glu His His His Phe Asn His Ala Val
380          370          375          380
383 Met Ile Leu Gln Ser Glu Gly His Asn Ile Phe Ala Asn Leu Ser Ser
384 385          390          395          400
387 Lys Glu Tyr Ser Asp Leu Met Gln Leu Leu Lys Gln Ser Ile Leu Ala
388          405          410          415
391 Thr Asp Leu Thr Leu Tyr Phe Glu Arg Arg Thr Glu Phe Phe Glu Leu
392          420          425          430
395 Val Ser Lys Gly Glu Tyr Asp Trp Asn Ile Lys Asn His Arg Asp Ile
396          435          440          445
399 Phe Arg Ser Met Leu Met Thr Ala Cys Asp Leu Gly Ala Val Thr Lys
400          450          455          460
403 Pro Trp Glu Ile Ser Arg Gln Val Ala Glu Leu Val Thr Ser Glu Phe
404 465          470          475          480
407 Phe Glu Gln Gly Asp Arg Glu Arg Leu Glu Leu Lys Leu Thr Pro Ser
408          485          490          495
411 Ala Ile Phe Asp Arg Asn Arg Lys Asp Glu Leu Pro Arg Leu Gln Leu
412          500          505          510
415 Glu Trp Ile Asp Ser Ile Cys Met Pro Leu Tyr Gln Ala Leu Val Lys
416          515          520          525
419 Val Asn Val Lys Leu Lys Pro Met Leu Asp Ser Val Ala Thr Asn Arg
420          530          535          540
423 Ser Lys Trp Glu Glu Leu His Gln Lys Arg Leu Leu Ala Ser Thr Ala
424 545          550          555          560
427 Ser Ser Ser Ser Pro Ala Ser Val Met Val Ala Lys Glu Asp Arg Asn
428          565          570          575

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431 &lt;210&gt; SEQ ID NO: 4

432 &lt;211&gt; LENGTH: 1925

433 &lt;212&gt; TYPE: DNA

434 &lt;213&gt; ORGANISM: Homo sapiens

436 &lt;400&gt; SEQUENCE: 4

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441 gctttgctag aggtggttaa tgacctcttt gaagaacaga ctgacctgga gaaaattgtc      180
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**VERIFICATION SUMMARY**

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